

## BEST AVAILABLE COPY

INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4835 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-976-259-58

Alignment Scores:  
Pred. No.: 0.00929 Length: 4835  
Score: 108.00 Matches: 59  
Percent Similarity: 31.69% Conservative: 31  
Best Local Similarity: 20.77% Mismatches: 86  
Query Match: 6.09% Indels: 108  
Gaps: 11

US-09-848-852A-3 (1-332) x US-08-976-259-58 (1-4835)

QY 42 LeupheglnGlySerAspLeuGlnMetAlaGlnGluAlaGlnArgProGlnGluLysAla 61  
DB 1350 CTATTTCCCTGCTGCGCTAGTATGTGAGAGTGTGACACCGACTTGGTGAAT 1409  
QY 62 GlnHisSerProLeuArgGlnGlnHisVal-----ThCysValGlnSerIle--- 78  
DB 1410 CAAAGCCACAAATTACTGTCATATGACATATTTTACGTAGCTGCCAGACATAGAC 1469  
QY 79 LeuAspGlnPheLeuGlnThrTyrlGlySerLeuIleProLeuSerThrAspGluValVal 98  
DB 1470 CTGCTGATTTATATAGATGCTATGATGATTTTATATGCGCATGAAATCGCAT 1520  
QY 99 GlnLysLeuGlnAspIlePheGlnGlnGlnPheSerThrProSerArgLysGlnLysVal 118  
DB 1521 ACCAATTTGTCAGATTTTTCCTGAAAAGTTTCAGAGTACAGATGTCAGCGCTATGCA 1580  
QY 119 LeuGlnLeuIleGlnSerTyrlGlnArgMetProGlnAlaMetValArgLysPheArg 138  
DB 1581 TTG----- 1583  
QY 139 ValAlaTyrlLysArgHisValLeuThrMetAspAspLeuGlnTyrlLeuTyrlGlnAsn 158  
DB 1584 ----- 1586  
QY 159 TrpLeuAsn----- 161  
DB 1587 TGGCCAAATTTTGGTTTCAGTGTGATGCTTCTGGAAGCGGTTGTTATGACGT 1646  
QY 162 -----AspGlnValMetAsnMetTyrlGlnAspLeuValMetAspThrVal 176  
DB 1647 TTTACCTATGCTGCCCCCAATCCTTTAAAGTTCATCACTCAAAAAGCGTGTCAA 1706  
QY 177 ProGlnLysValHisPheAsnSerPhePheTyrlAspLysLeuArgThrLysGlnTyrl 196  
DB 1707 CCGAGACAGATTAAACCGTTTCATATATCCGATTAATGCTGATTTGCTTATGTCGATAT 1766  
QY 197 AspGlnValLysArgTyrlPheAsnValAspIlePheAsnLysGlnLeuLeuIle 216  
DB 1767 -----ATCATGATTTGGGTCGCGATTTGATTTCTGAC 1799  
QY 217 ProIleHis-----LeuGlnValHisTrpSerLeuIleSerValAspVal 231  
DB 1800 CCGAGGCGATGTAATGGGTTAGTGTAGTACTGAGTGGAGCGGTGTCAGGTA----- 1853  
QY 232 ArgArgArgThrIleThrTyrlPheAspSerGlnArgHisLeuAsnArgArgCysProLys 251  
DB 1854 -----AATCACTATGACGTTAA 1871  
QY 252 His-----IleAlaLysTyrlLeuGlnAlaGlnValLysLysAspArg 266  
DB 1872 TCACTTGAGAAATCTTGTGGGCAACATCTGCTGTAGTGTGCTGCACTGCAATCGA 1931  
QY 267 LeuAspPheHisGlnGlnTyrlPheLysGlnTyrlPheLysMetAsnValAlaArgGlnAsn 286  
DB 267 -----AAAGATTATTTCAAG-----GCACATGATCGTAAT 1970

QY 287 AspSerAspCys 290  
DB 1971 GATGAGAGCTGC 1982

RESULT 2  
US-08-375-709-2

Sequence 2, Application US/08375709  
Patent No. 5683898

GENERAL INFORMATION:  
APPLICANT: YAZAWA, Kazunaga

APPLICANT: YAMADA, Akiko

APPLICANT: KATO, Seishi

APPLICANT: KONDO, Kiyoaki

TITLE OF INVENTION: Gene Coding for Elcosapentaenoic Acid

TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

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COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/375,709

FILING DATE: 20-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,251

FILING DATE: 14-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-147945

FILING DATE: 15-MAY-1992

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INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1983 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Shewanella putrefaciens SCRC-2874 (FERM

ORGANISM: BP-1625)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1983

NAME/KEY: mat\_peptide

LOCATION: 1..1983

Alignment Scores:

Pred. No.: 0.169

Score: 93.00

Percent Similarity: 32.96%

Best Local Similarity: 20.95%

Query Match: 5.25%

DB: 1

Length: 1983

Matches: 75

Conservative: 43

Mismatches: 117

Indels: 123

Gaps: 19

